

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2002, 01:18:04 ; Search time 10687.2 seconds
(without alignments)
3033.262 Million cell updates/sec

Title: US-08-913-842-2

Sequence: 1 AAGCTTCAAGTAACTCTCTG.....TGAACACAAAGAAATG 1965

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

1 number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBankl:*

1: gb_da:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_cm:*

20: em_ov:*

21: em_pat:*

22: em_ph:*

23: em_pl:*

24: em_ro:*

25: em_sts:*

26: em_sy:*

27: em_un:*

28: em_vi:*

29: em_ba:*

30: em_fun:*

31: em_hum:*

32: em_in:*

33: em_cm:*

34: em_ov:*

35: em_pat:*

36: em_ph:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	178	9.1	1319	8	VIREXT5	D16458 V.angularis
2	115.2	5.9	136098	2	AC006970	AC006970 Homo sapi
3	114.8	5.8	12029	3	AE001422	AE001422 Plasmid
4	114.6	5.8	86827	3	PFMAL3P5	AL034556 Plasmid
5	112.4	5.7	136098	9	AC006970	AC006970 Homo sapi
6	112.2	5.7	259474	9	HDAC004605	AC004605 Homo sapi
7	112	5.7	196152	2	AC079796	AC079796 Homo sapi
8	111.6	5.7	158398	2	AC011146	AC011146 Homo sapi
9	110.2	5.6	86827	3	PFMAL3P5	AL034556 Plasmid
10	110	5.6	161991	2	AC055860	AC055860 Homo sapi
11	109.6	5.6	158398	2	AC011146	AC011146 Homo sapi
12	109.2	5.6	115218	9	HS159A1	AL034556 Plasmid
13	108.8	5.5	193302	2	AC021992	AC021992 Homo sapi
14	108.6	5.5	67970	3	PFMAL1P3	AL034556 Plasmid
15	108.4	5.5	142339	2	AL390835	AL034556 Plasmid
16	108.2	5.5	175223	2	AC004617	AC004617 Homo sapi
17	108	5.5	14867	3	AE001398	AE001398 Plasmid
18	108	5.5	157176	2	AC084716	AC084716 Homo sapi
19	107.6	5.5	326924	2	AC093082	AC093082 Homo sapi
20	107.4	5.5	39347	9	AL135806	AL135806 Homo sapi
21	107.4	5.5	140455	2	AL356793	AL135806 Homo sapi
22	107.2	5.5	201312	2	AC067900	AL135806 Homo sapi
23	107.2	5.5	156133	2	AL593856	AL593856 Homo sapi
24	107	5.4	176174	2	AC007483	AL593856 Homo sapi
25	106.8	5.4	128603	2	AL356272	AL593856 Homo sapi
26	106.6	5.4	172805	9	AC066608	AL593856 Homo sapi
27	106.6	5.4	176087	3	AC005089	AC066608 Homo sapi
28	106.4	5.4	4601	3	DMU11584	AC005089 Homo sapi
29	106.4	5.4	19517	2	DMU37541	U11584 Drosophila
30	106.4	5.4	104992	2	AC005504	U11584 Drosophila
31	106.4	5.4	169546	2	AC004157	AC005504 Plasmid
32	106.2	5.4	120029	2	HS282810	AC004157 Plasmid
33	106.2	5.4	199335	2	AC092665	AL132672 Homo sapi
34	106	5.4	106763	9	AP002091	AC092665 Homo sapi
35	105.8	5.4	205094	2	CNS01RHO	AP002091 Homo sapi
36	105.6	5.4	142339	2	AL390835	AL162191 Homo sapi
37	105.6	5.4	194212	2	AC092148	AL390835 Homo sapi
38	105.4	5.4	36977	2	AC092304	AC092148 Homo sapi
39	105.4	5.4	67970	3	PFMAL1P3	AC092304 Homo sapi
40	105.4	5.4	161286	2	AC025120	AL031746 Plasmid
41	105.4	5.4	175223	9	AC004617	AC025120 Homo sapi
42	105.2	5.4	326924	2	AC093082	AC004617 Homo sapi
43	104.8	5.3	169794	2	AC004688	AC093082 Homo sapi
44	104.8	5.3	172666	2	AC046181	AC004688 Plasmid
45	104.8	5.3	183385	2	AL589943	AC046181 Homo sapi

ALIGNMENTS

RESULT 1

VIREXT5 1319 bp mRNA 01-FEB-2000

LOCUS V.angularis mRNA for endo-xyloglucan transferase, complete cds.

DEFINITION D16458

ACCESSION D16458.1 GI:457572

VERSION

KEYWORDS

SOURCE

ORGANISM

Vigna

endoglycanotransferase; endo-xyloglucan transferase; extracellular protein; glycosylated protein; molecular grafting between xyloglucan polymers; novel glycosyltransferase.

Vigna angularis seedlings cDNA to mRNA.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

REFERENCE 1 (bases 1 to 1319)

AUTHORS Okazawa,K., Sato,Y., Nakagawa,T., Asada,K., Kato,I., Tomita,E. and Nishitani,K.

TITLE Molecular cloning and cDNA sequencing of endoxyloglucan transferase, a novel class of glycosyltransferase that mediates

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

molecular grafting between matrix polysaccharides in plant cell walls
J. Biol. Chem. 268 (34), 25364-25368 (1993)
94064597
2 (bases 1 to 1319)
Nishitani, K.
Direct Submission
Submitted (17-JUN-1993) Kazuhiko Nishitani, Kagoshima University,
College of Liberal Arts, Department of Biology, Kagoshima,
Kagoshima 890, Japan (E-mail: nishitane@kagoshima-u.ac.jp,
Tel:0992-85-8938, Fax:0992-85-8946)
Submitted (17-JUN-1993) to DDBJ by:
Kazuhiko Nishitani
Department of Biology
College of Liberal Arts
Kagoshima University
Kagoshima 890
Japan
Phone: 0992-85-8938
Fax: 0992-85-8946.

COMMENT

JRES
source

Location/Qualifiers
1.1319

/organism="Vigna angularis"

/db_xref="taxon:3914"

/dev_stage="seedlings"

/gene="ext"

/gene="ext"

/gene="ext"

/gene="ext"

/codon_start=1

/product="endo-xyloglucan transferase"

/protein_id="BA03925.1"

/db_xref="GI:469510"

/translation="MGSSLMTCLLILSLASASPAANPRPIDVPEGRNVPYTFADHI
KYLNGSEIQLDKYGTGTFQSGSYLFHGSMTKLYPGDSAGTVAFYLSNNAE
HDEIDPEFGNRTGOPYILOTWVPGKREORIYIMDPPTOYHRSVILMNIOY
EYDDYPIRFVFNKSNLDGVKFPFNPKIYNSLWADDMATGGLKEDMSRAPTIAS
YKGFHIDGCEASVNAKFCDTGCKRMDDEFRDLDAOMOKLAWRNKITYNYCTDR
KRYSOVPECTYDRDI"

BASE COUNT 399 a 276 c 261 g 383 t
ORIGIN

Query Match 9.5%; Score 178; DB 8; Length 1319;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1698 ATGAACACAAATACGAGTCTCAATCAATGAACATTAATTAATTCAGTTA 1757
|||||
1 ATGAACACAAATACGAGTCTCAATCAATGAACATTAATTAATTCAGTTA 60
OY 1758 AAGTCATTGATCAGAACAGCAGTGAAGTTAGTAAAGCGGTATAGTGCGAGCAG 1817
|||||
Db 61 AAGTCATTGATCAGAACAGCAGTGAAGTTAGTAAAGCGGTATAGTGCGAGCAG 120
OY 1818 AGTGTGCGCTATATATACCTTTGGAATGCACAAAGTTGAACAAAGAAAATG 1875
|||||
Db 121 AGTGTGCGCTATATATACCTTTGGAATGCACAAAGTTGAACAAAGAAAATG 178

RESULT 2
CONSIRHQ
LOCUS
DEFINITION
PROGRESS *** in ordered pieces.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL162191.5 GI:12001743
HTG: HTGS_PHASE2; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 205094)
Genoscope.
Direct Submission
Submitted (28-DEC-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jan 1, 2001 this sequence version replaced gi:9844068.

COMMENT

Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage, etc. even if efforts are made to eliminate these
contaminating sequences. The following BAC sequence is oriented
from the 17 to the SP6 end.
Upstream BAC (overlapping the T7 end) : C-2350B12
Downstream BAC (overlapping the SP6 end) : C-2174H20 (AC-AL356806)
Summary Statistics
Assembly program: Phrap, version 2.0
Quality coverage: 7.17x in Q20 bases; sum-of-contigs

Overall quality chart :

Range : bases
0 - 153
1 - 9 : 116
10 - 19 : 634
20 - 29 : 1039
30 - 39 : 2796
40 - 49 : 9475
50 - 59 : 20955
60 - 69 : 17443
70 - 79 : 22605
80 - 89 : 42026
90 - 99 : 87852

Percentage of bases with a quality value >= 40 : 97 %
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

Source
1.205094
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-349D8"
/clone_1b="RPCI-11"
122135..122397
/note="matching EMBL:Z51462
RHD:RH31306
dbSTS:SPS19836
Identified using the e-PCR software (G. Schuler)"
158123..158266
/note="matching EMBL:G33165
RHD:RH42760
dbSTS:STS36190
Identified using the e-PCR software (G. Schuler)"
BASE COUNT 61484 a 44117 c 40393 g 59100 t
ORIGIN

Query Match 9.2%; Score 173.2; DB 2; Length 205094;
Best Local Similarity 46.6%; Pred. No. 4.1e-11;
Matches 804; Conservative 0; Mismatches 896; Indels 22; Gaps 7;

Wed Jan 9 10:11:45 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2002, 19:07:28 ; Search time 10687.2 Seconds

(without alignments)
2894.334 Million cell updates/sec

Title: US-08-913-842-1

Perfect score: 1875
Sequence: 1 AACCTTTTGCACATTTTG.....TGAAACACAAGAAAAATG 1875

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Number of hits satisfying chosen parameters: 2344280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.om:*
20: em.or:*
21: em.ov:*
22: em.pat:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
27: em.sy:*
28: em.un:*
29: em.vi:*
30: em.hugo.hum:*
31: em.hugo.inv:*
32: em.hugo.rod:*
33: em.htg.hum:*
34: em.htg.inv:*
35: em.htg.rod:*
36: em.htg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	9.5	1319	8	VIREXTS
2	173.2	9.2	205094	2	CNS01RHQ
3	159.4	8.5	86827	3	PFMAL3P5
4	156.6	8.4	158398	2	AC011146
5	155.4	8.3	4601	3	DMU1584
6	155.4	8.3	19517	3	DMU37541
7	154.2	8.2	4601	3	DMU1584
8	154.2	8.2	19517	3	DMU37541
9	153.4	8.2	14867	3	DMU01398
10	151.6	8.1	156933	2	AC026839
11	151.4	8.1	183584	9	AC012492
12	151.2	8.1	143331	9	AC091214
13	150.4	8.0	14867	3	AE001398
14	150.4	8.0	67970	3	PFMAL1P3
15	149.2	8.0	176174	9	AC007483
16	148.6	7.9	67970	3	PFMAL1P3
17	147.6	7.9	104992	2	AC005504
18	147.6	7.9	169546	2	AC004157
19	146	7.8	86827	3	PFMAL1P5
20	144.8	7.7	104992	2	AC005504
21	144.8	7.7	169546	2	AC004157
22	143.6	7.7	158398	2	AC011146
23	141.8	7.6	175223	9	AC092304
24	141.2	7.5	326924	2	AC093082
25	138.6	7.4	12266	2	AC046181
26	138.4	7.4	36977	2	AC092304
27	138.2	7.4	173349	2	AL596253
28	137.8	7.3	188930	2	AC091742
29	137	7.3	218078	2	AC068138
30	136.6	7.3	176174	9	AC007483
31	136.6	7.3	326924	2	AC093082
32	136	7.3	199551	2	AC006281
33	134.8	7.2	188930	2	AC091742
34	134.6	7.1	103649	2	AL445219
35	133.6	7.1	36977	2	AC092304
36	133.4	7.1	106650	9	AC007708
37	133	7.1	173349	2	AL596253
38	132.8	7.0	136098	9	AC006970
39	132	7.0	172666	2	AC046181
40	131.2	7.0	181581	7	AC026621
41	130.8	7.0	259474	9	HUAC004605
42	130.4	6.9	14001	3	PFMAL1P3
43	128.6	6.9	106763	9	AP002091
44	128.6	6.8	142239	2	AL390835
45	128				

ALIGNMENTS

RESULT	1				
VIREXTS					
LOCUS	VIREXTS	1319 bp	mRNA	PLN	01-FEB-2000
DEFINITION	V. angularis	mRNA for endo-xyloglucan transferase, complete cds.			
ACCESSION	D16458				
VERSION	D16458.1	GI:457572			
KEYWORDS	endo-glycanotransferase; endo-xyloglucan transferase; extracellular protein; glycosylated protein; molecular grafting between xyloglucan polymers; novel glycosyltransferase.				
SOURCE	Vigna angularis seedlings cDNA to mRNA.				
ORGANISM	Vigna angularis				
REFERENCE	1 (bases 1 to 1319)				
AUTHORS	Okazawa,K., Sato,Y., Nakagawa,T., Asada,K., Kato,I., Tomita,E. and Nishitani,K.				
TITLE	Molecular cloning and cDNA sequencing of endoxyloglucan transferase, a novel class of glycosyltransferase that mediates				